

Best Local Similarity 100.0%;
Matches 2932; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Scoring table: TABLE default
Gap 6

RESULT 2
ID Q66636 standard; cDNA; 2932 BP.
AC Q66636;
DT 19-JAN-1995 (first entry)
DE Human Activin receptor-like kinase 3 (hALK-3) cDNA.

RESULT 3
ID Q66640 standard; cDNA; 2070 BP.
AC Q66640;
DT 20-JAN-1995 (first entry)
DE Mouse Activin receptor-like kinase 3 (mALK-3) cDNA.
KW serine threonine kinases; activin receptors; Act R; superfamily;
KW transforming growth factor; TGF; diagnostics; detection; therapy;
KW rheumatoid arthritis; glomerular nephritis; fibrosis; ss.

RESULT 4
ID Q90184 standard;
AC Q90184;
DT 01-NOV-1995 (first entry)
DE BRK-1 DNA.

RW BRK-1; BMP receptor kinase protein-1; bone morphogenetic protein; ds.
OS Mus sp.
FH Key Location/Qualifiers
FT CDS 11..1609

FT /*tag=^A
FT sig_peptide 11..79
FT /*tag=^B
FT mat_peptide 80..1606
FT /*tag=^C
PN W09514778-A.
PD 01-JUN-1995.
PR 23-NOV-1994; U13534.

PA (PROC) PROCTER & GAMBLE CO.
PI Cook JS, Correa PE, Koenig BB, Rosenbaum JS, Ting J;
DR WPI; 95-206935/27.
DR P-PSDB; R74343.
PT New bone morphogenetic protein receptor kinase protein - used for
PT identifying cpds capable of binding it and for developing therapeutic
PT agents and detection system(s).
PT Claim 3; Page 29-32; 49pp; English.
CC A cDNA library prepared from NIH3T3 poly-A RNA was screened with
CC J159 PCR fragment to isolate clone BRK-1 (sequence given in
CC Q90184) encoding full-length BMP receptor kinase protein (R74343).
CC Vectors including the DNA were used to express recombinant BRK-1 in
CC CHO and COS-7 hosts.
SQ Sequence 2402 BP; 676 A; 482 C; 540 G; 704 T;

Query Match 47.1%; Score 1380; DB 14; Length 2402;
Best Local Similarity 89.6%; Pred. No 0.00e+00;
Matches 1596; Conservative 0; Mismatches 180; Indels 6; Gaps 5;

MDsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm
Run on: Thu Jun 26 00:21:54 1997; MasPar time 1832.45 Seconds
Tabular output not generated.

Title: >US-08-436-265-5
Description: (1-2932) From US08436265.seq
Perfect Score: 2932
N.A. Sequence: 1 GCTTCGGCGCCGAGGGCTGGA.....GCTTATTGCAAATCACCC 2932
Comp: CGAGGCGGGTCCGACT.....CGAAATAAACGTTAGTGGG

Scoring table: TABLE default
Gap 6

Searched: 887282 seqs, 320523384 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: EST-STS
SUMMARIES

RESULT
ID Q66640 standard; cDNA; 2070 BP.
AC Q66640;
DT 20-JAN-1995 (first entry)
DE Mouse Activin receptor-like kinase 3 (mALK-3) cDNA.
KW serine threonine kinases; activin receptors; Act R; superfamily;
KW transforming growth factor; TGF; diagnostics; detection; therapy;
KW rheumatoid arthritis; glomerular nephritis; fibrosis; ss.

RESULT
ID W39552
LOCUS zc18944.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone
DEFINITION 322710 5' similar to gb:222535_cds1 SERINE/THREONINE-PROTEIN KINASE
RECEPTOR R5 PRECURSOR (HUMAN);
RESULT 2
LOCUS HSC22A061
DEFINITION H. sapiens partial cDNA sequence; clone c-2za06.
ACCESSION F11592
NID 9705894

RESULT 3
LOCUS W15390
DEFINITION zc18944.s1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone
322710 3'.
ACCESSION W15390
KEYWORDS EST.
NID 91289800
RESULT 4
LOCUS W15390
DEFINITION zc18944.s1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone
322710 3'.
ACCESSION W15390
NID 91289800
KEYWORDS EST.

RESULT 5
LOCUS H97091
DEFINITION yv89a08.r1 Homo sapiens cDNA clone 249878 5'.
ACCESSION H97091
NID 91114134
KEYWORDS EST.

Run on: Tue Jun 24 17:49:57 1997; MasPar time 11.29 Seconds
Tabular output not generated.
Title: >US-08-436-265-6
Description: (1-532) from US08436265.pep
Perfect Score: 3981

Scoring table: TABLE default
Gap 6

Searched: 887282 seqs, 320523384 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: EST-STS
SUMMARIES

RESULT
ID Q66640 standard; cDNA; 2070 BP.
AC Q66640;
DT 20-JAN-1995 (first entry)
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Tabular output not generated.
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Description: (1-532) from US08436265.pep
Perfect Score: 3981

Scoring table: TABLE default
Gap 6

Searched: 887282 seqs, 320523384 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

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Post-processing: Minimum Match 0%
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Run on: Tue Jun 24 17:49:57 1997; MasPar time 11.29 Seconds
Tabular output not generated.
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Post-processing: Minimum Match 0%
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Run on: Tue Jun 24 17:49:57 1997; MasPar time 11.29 Seconds
Tabular output not generated.
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Description: (1-532) from US08436265.pep
Perfect Score: 3981

Scoring table: TABLE default
Gap 6

Searched: 887282 seqs, 320523384 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

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RECEPTOR R5 PRECURSOR (HUMAN);
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Run on: Tue Jun 24 17:49:57 1997; MasPar time 11.29 Seconds
Tabular output not generated.
Title: >US-08-436-265-6
Description: (1-532) from US08436265.pep
Perfect Score: 3981

Scoring table: TABLE default
Gap 6

Searched: 887282 seqs, 320523384 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: EST-STS
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RESULT
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Run on: Tue Jun 24 17:49:57 1997; MasPar time 11.29 Seconds
Tabular output not generated.
Title: >US-08-436-265-6
Description: (1-532) from US08436265.pep
Perfect Score: 3981

Scoring table: TABLE default
Gap 6

Searched: 887282 seqs, 320523384 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: EST-STS
SUMMARIES

RESULT
ID Q66640 standard; cDNA; 2070 BP.
AC Q666

RESULT 5

ID R96201 standard; Protein; 532 AA.

AC R96201;

DT 22-AUG-1996 (first entry)

DE Bone morphogenetic protein type-I receptor kinase-1.

KW Mouse; bone morphogenetic protein receptor kinase-1;

KW bone morphogenetic protein receptor kinase-3; antibody; diagnostic;

KW bone disorder; osteogenic; bone morphogenetic protein-agonist;

KW drug screening; reporter gene; bone morphogenetic protein-antagonist;

KW hormone-responsive element.

OS Mus musculus.

Key

Location/Qualifiers

Peptide 216..221

/note= "Conserved BRK-1 motif"

Peptide 398..421

/note= "Peptide used to raise antibody"

PN W09614412-A2.

PD 17-MAY-1996.

PF 30-OCT-1995; U14085.

PR 04-NOV-1994; US-334179.

PA (PROC) PROCTER & GAMBLE CO.

PN Nohno T, Rosenbaum JS;

PD 23-MAR-1995.

PF 07-SEP-1994; U10080.

PR 17-SEP-1993; US-123934.

PA (GEMY) GENETICS INST INC.

PI Celeste AJ, Thies RS, Woynay JM, Yamaji N;A;

Query Match 98.0%; Score 3900; DB 13; Length 532;

Best Local Similarity 97.2%; Pred. No. 0.00e+00;

Matches 517; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

Qy 481 PIVSNRWNSD 491

PI R85209 standard; Protein; 502 AA.

AC R85209;

DT 13-FEB-1996 (first entry)

DE Mouse ALK-6.

KW ALK-3; OP1 binding receptor; osteogenic protein 1; morphogenesis;

KW morphogen; agonist; antagonist.

OS Mus sp.

Key

Location/Qualifiers

Peptide 1..22

/label= Sig_Peptide

Domain 23..122

/label= Extracellular domain

Domain 123..205

/label= Transmembrane domain

Domain 206..497

/label= Intracellular domain

/note= "serine/threonine-kinase domain"

PN W0953003-A2.

PD 09-NOV-1995.

PF 28-APR-1995; U05467.

PR 29-APR-1994; US-234628.

PA (CREA-) CREATIVE BIOMOLECULES INC.

PA (LUDW-) LUDWIG INST CANCER RES.

PI Dijke PT, Heldin C, Miyazano K, Sampath KT;

DR WPI; 95-393076/50.

DR N-PSDB; T06032.

PT Identifying osteogenic protein-1 receptor-binding analogue - useful

in the design of morphogen agonists and antagonists for therapeutic,

diagnostic and experimental purposes

PT Claim 1; Page 73-76; 95pp; English.

PS The Type-I cell surface receptors ALK-2, ALK-3 and ALK-6 (Given in

CC The Type-I cell surface receptors ALK-2, ALK-3 and ALK-6 (Given in

CC R85206, R85207 and R85209) have specific binding affinity for

CC osteogenic protein 1 (OP1) and OP1-related analogues. The

CC receptors are used to identify novel morphogen receptor binding

CC analogues useful in drug design.

SQ Sequence 502 AA;

Query Match 69.3%; Score 2757; DB 14; Length 502;

Best Local Similarity 71.3%; Pred. No. 3.26e-264;

Matches 363; Conservative 76; Mismatches 61; Indels 5; Gaps 5;

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Jun 24 17:48:18 1997; MasPar time 19.20 Seconds

78.9-840 Million cell updates/sec

Tabular output not generated.

Title: >US-08-436-255-6

Description: (1-532) from US08436265.pop

Perfect Score: 3981

Sequence: 1 MTQLIYIYLGLFISR.....TALRIKTLAKMIVESQDVKI 532

Scoring table: PAM 150

Gap 11

Searched: 89912 seqs, 28507787 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: pir50

1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3

8:unann4 9:unann5 10:unann6 11:unann7 12:unann8

13:unann9 14:unann10 15:unenc 16:unrev

Statistics: Mean 49.071; Variance 114.924; scale 0.427

PI Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result %

No. Score Query Match Length DB ID Description

1 3981 100.0 532 13 S3718 3 ALK-3 protein - huma

2 3981 100.0 532 13 I3716 3 ALK-3 - human

3 3915 98.3 532 14 A5623 8 bone morphogenetic p

4 3900 98.0 532 14 JC2387 bone morphogenetic p

5 3615 90.8 500 14 B5623 8 bone morphogenetic p

6 3139 78.8 527 12 A54985 BMP receptor precurs

7 2757 69.3 502 14 A5344 4 activin receptor-lik

8 2757 69.3 502 14 JC2491 serine/threonine

9 2747 69.0 502 13 A56683 receptor protein kin

10 1762 44.3 503 13 A49432 activin receptor-lik

RESULT 3

ENTRY A56238 #type complete

TITLE bone morphogenetic protein receptor BRK-1 - mouse

ALTERNATE NAMES ALK-3 protein; BMP receptor

ORGANISM #formal_name Mus musculus #common_name house mouse

DATE 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change

06-Sep-1996

* A56238; S40158; I48242; I49543
 * A56238
 * #authors Koenig, B.B.; Cook, J.S.; Wolsing, D.H.; Ting, J.; Tiesman, J.P.; Correa, P.E.; Olson, C.A.; Pecquet, A.L.; Ventura, F.; Grant, R.A.; Chen, G.X.; Wrama, J.L.; Massague, J.; Rosenbaum, J.S.
 * #journal Mol. Cell. Biol. (1994) 14:5961-5974
 * #title Characterization and cloning of a receptor for BMP-2 and BMP-4 from NIH 3T3 cells.
 * #accession A56238
 * #status preliminary
 * ##molecule_type mRNA
 * ##residues 1-532 ##label KOE
 * ##cross-references GB:U04672
 * REFERENCE S40158
 * #authors Mizazono, K.; Moren, A.; Grimsby, S.; Ichijo, H.; Heldin, C.; ten Dijke, P.
 * #submission submitted to the EMBL Data Library, June 1993
 * #description ALK-3 and ALK-6: the closely related members in the serine/chreosine kinase receptor family.
 * #accession S40158
 * #status preliminary
 * ##molecule_type mRNA
 * ##residues 1-532 ##label MIY
 * REFERENCE I48241
 * #authors Dewulf, N.; Verschueren, K.; Lonnroy, O.; Moren, A.; Grimsby, S.; Vande Spiegle, K.; Miyazono, K.; Huybrecht, D.; Ten Dijke, P.
 * #journal Endocrinology (1995) 136:2652-2663
 * #title Distinct spatial and temporal expression patterns of two types of I receptors for bone morphogenetic proteins during mouse embryogenesis.
 * #cross-references MUID:952669711
 * #accession I48242
 * #status preliminary; translated from GB/EMBL/DBBJ
 * ##molecule_type mRNA
 * ##residues 1-532 ##label 1 RES
 * ##cross-references EMBL:Z23154; NID:9437868; CDS_PID:9437869
 * REFERENCE I49543
 * #authors Suzuki, A.; Thies, R.S.; Yamaji, N.; Song, J.J.; Wozney, J.; Murakami, K.; Kung, H.
 * #journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:10255-10259
 * #title A truncated bone morphogenetic protein receptor affects dorsal-ventral patterning in the early Xenopus embryo.
 * #cross-references MUID:95024092
 * #accession I49543
 * #status translated from GB/EMBL/DBBJ
 * ##molecule_type mRNA
 * ##residues 1-532 ##label RE2
 * ##cross-references GB:DI6250; NID:9577633; CDS_PID:9577634
 * CLASSIFICATION #superfamily protein kinase homology
 * KEYWORDS phosphotransferase; transmembrane protein
 * FEATURE
 * #domain signal sequence #status predicted #label SIG
 * 1-23
 * 232-528 #domain protein kinase homology #label KIN
 * SUMMARY #length 532 #molecular_weight 60063 #checksum 6896
 * #cross-references GB:DI6250; NID:9577633; CDS_PID:9577634
 * CLASSIFICATION #superfamily protein kinase homology
 * KEYWORDS phosphotransferase; transmembrane protein
 * FEATURE
 * #domain signal sequence #status predicted #label SIG
 * 1-23
 * 232-528 #domain protein kinase homology #label KIN
 * SUMMARY #length 532 #molecular_weight 60063 #checksum 6896
 * Query Match 98.3%; Score 3915; DB 14; Length 532;
 * Best Local Similarity 98.1%; Pred. No. 0.00e+00;
 * Matches 522; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
 * Result No. Score Match Length DB ID Description
 * 1 3981 100.0 532 5 KIR5_HUMAN SERINE/THREONINE-PROT 0.00e+00
 * 2 3915 98.3 532 5 KIR5_MOUSE SERINE/THREONINE-PROT 0.00e+00
 * 3 2757 69.3 502 5 KIR6_MOUSE SERINE/THREONINE-PROT 0.00e+00
 * 4 2747 69.0 502 5 KIR6_CHICK SERINE/THREONINE-PROT 0.00e+00
 * 5 1762 44.3 503 5 KIR4_HUMAN SERINE/THREONINE-PROT 0.00e+00
 * 6 1737 43.6 501 5 KIR4_RAT SERINE/THREONINE-PROT 0.00e+00
 * 7 1638 41.1 509 5 KIR1_RAT SERINE/THREONINE-PROT 0.00e+00
 * 8 1630 40.9 509 5 KIR1_HUMAN SERINE/THREONINE-PROT 0.00e+00
 * 9 1617 40.6 509 5 KIR1_MOUSE SERINE/THREONINE-PROT 0.00e+00
 * 10 1614 40.5 505 5 KIR2_HUMAN SERINE/THREONINE-PROT 0.00e+00
 * Statistics: Mean 50.780; Variance 83.714; scale 0.607
 * Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
 * SUMMARIES

! - SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-PROTEIN KINASES. STRONG, TO ACTIVIN RECEPTORS.									
1612	40.5	505	5	KIR2_RAT	SERINE/THREONINE-PROT	0.00e+00	CC	CC	CC
1509	37.9	503	5	KIR3_HUMAN	SERINE/THREONINE-PROT	0.00e+00	DR	DR	DR
1498	37.6	505	5	KIR3_RAT	SERINE/THREONINE-PROT	0.00e+00	EMBL	Z23154; G43786;9;	-
852	21.4	514	1	AVR2_XENLA	ACTIVIN RECEPTOR TYPE	1.21e-171	DR	D16250; G57763;4;	-
842	21.2	669	3	DAF1_CAEEL	CELL-SURFACE RECEPTOR	3.66e-169	DR	U04672; G53836;3;	-
826	20.7	513	1	AVR2_HUMAN	ACTIVIN RECEPTOR TYPE	3.39e-165	DR	S40158; S40158;	-
826	20.7	513	1	AVR2_MOUSE	ACTIVIN RECEPTOR TYPE	3.39e-165	DR	PS00107; PROTEIN_KINASE_ATP.	-
823	20.5	513	1	AVR2_RAT	ACTIVIN RECEPTOR TYPE	1.88e-164	DR	PS00108; PROTEIN_KINASE_ST.	-
816	20.5	636	11	YQD2_CAEEL	PUTATIVE SERINE/THREO	1.02e-162	DR	PS50011; PROTEIN_KINASE_DOM.	-
765	19.2	511	1	AVR2_XENLA	ACTIVIN RECEPTOR TYPE	4.07e-150	KW	RECEPTOR_TRANSFERASE; SERINE/THREONINE-PROTEIN KINASE; ATP-BINDING:	-

1 HUMAN STANDARD; PRT; 532 AA.

RESULT	3			
ID	KIR6	MOUSE	STANDARD;	PRT;
2	2	2		502
3	3	3	AA.	

AN
DT 01-JUN-1994 (REL. 29, CREATED)
DT 01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (DET. 32, LAST ANNOTATION UPDATE)

DE SERINE/THREONINE- PROTEIN KINASE RECEPTOR R6 PRECURSOR (EC 2.7.1.37)
 DE (SKR6) (ACTIVIN RECEPTOR-LIKE KINASE 6) (ALK-6).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC PRIMATES; HOMO SAPIENS.

OC
RN
RP
DY
SEQUENCE FROM N.A.
MED. T.D. 043000.C
DOLPHIN, KODERIA.

RA TEN DILKE P., YAMASHITA H., ICHIJO H., FRANZEN P., LAIHO M.,
RA MIYAZONO K., HELDIN C.H.;
RA SCIENCE 264: 101-104 (1994);
RI

CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -!- SIMILARITY: THE CONSERVED CATALYTIC DOMAINS OF SER/THR-
 CC PROTEIN KINASES. STRONG, TO ACTIVIN RECEPTORS.
 DR EMBRY: 223143; G437871; -

DR PIR: A53444 ; A53444 .
DR PIR: S40159 ; S40159 .
DR HSSP: P01359 ; 1PCP .

DR PROSITE; PS00107; PROTEIN_KINASE_ATP.
DR PROSITE; PS00108; PROTEIN_KINASE_ST.
DR PROSITE; PS00101; PROTEIN_KINASE_DOM.
KW RECEPTOR; TRANSFERASE; SERINE/THREONINE-PROTEIN KINASE; ATP-BINDING;

KW	TRANSMEMBRANE	GLYCOPROTEIN;	SIGNAL.
FT	SIGNAL	1	13
FT	CHAIN	14	502

FT	DOMAIN	1.4	1.26	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1.27	1.48	POTENTIAL.
FT	DOMAIN	1.49	5.02	CYTOSMERIC (POTENTIAL).
FT	DOMAIN	20.4	4.94	PROTEIN KINASE.

FT	NP_BIND	210	218	ATP (BY SIMILARITY).
FT	BINDING	231	231	ATP (BY SIMILARITY).
FT	ACT_SITE	332	332	ATP (BY SIMILARITY).
SQ	SEQUENCE	502 AA;	56944 MW;	D1EC67A0 CRC32;

Query Match 69.3%; Score 2757; DB 5; Length 502;
 Best Local Similarity 71.9%; Pred. No. 0.0e+00;

MPsrch_nm n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Sat May 24 07:04:02 1997; Mastar time 98.46 Seconds 851.271 Million cell updates/s
Tabular output not generated.

Title: Description: >US-08-4336-265-5
(1-2932) from US08436265.seq

RefSeq	2932	1	GCTCCGGGCCGAGGGCTGGA,	GCTTTATTGCAAATCACC
N.A. Sequence:			CGAAATTAACGTTTATGGGG	CGAAATTAACGTTTATGGGG
Comp:			CGAAGCGGGCTCCGACCT	CGAAGCGGGCTCCGACCT

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0
Searched: 53119 seqs, 14293498 bases x 2

Post-processing: Minimum Match 0%
Listing First 45 summaries

Database: n-issued
1:51 2:52 3:53 4:54 5:55 6:PCT90 7:PCT91 8:PCT92 9:PCT93
10:PCT94 11:PCT95 12:PCT96

Statistics: Mean 9.515; Variance 4.793; scale 1.985

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description	Pred. No.
1	2932	100.0	2932	11	PCT-US95-0	Sequence 5,	Applicatio	0.00e+00
2	1296	44.2	1813	10	PCT-US94-0	Sequence 1,	Applicatio	0.00e+00
3	509	17.4	2076	10	PCT-US94-1	Sequence 3,	Applicatio	0.00e+00
4	508	17.3	1952	11	PCT-US95-0	Sequence 7,	Applicatio	0.00e+00
5	255	8.7	1506	5	PCT-US94-1	Sequence 2,	Applicatio	8.06e-183
6	255	8.7	1506	5	PCT-US94-1	Sequence 2,	Applicatio	8.06e-183
7	252	8.6	1647	10	PCT-US94-1	Sequence 7,	Applicatio	2.52e-180
8	244	8.3	3238	10	PCT-US94-1	Sequence 5,	Applicatio	1.12e-173
9	241	8.2	1506	5	PCT-US94-1	Sequence 4,	Applicatio	3.45e-171
10	241	8.2	1506	5	PCT-US94-1	Sequence 4,	Applicatio	3.45e-171

RESULT 1
ID PCT-US95-05467-5 STANDARD; DNA; UNC; 2932 BP.
AC xxxxxx
DT 01-JAN-1900
DE Sequence 5, Application PC/TUSS9505467.
CC Sequence 5, Application PC/TUSS9505467
CC GENERAL INFORMATION:
CC APPLICANT:

CC TITLE OF INVENTION: MORPHOGENIC PROTEIN-SPECIFIC CELL
CC TITLE OF INVENTION: SURFACE RECEPTORS AND USES THEREFOR
CC NUMBER OF SEQUENCES: 15
Nmrch_PP protein - protein database search, using Smith-Waterman algorithm

Run on: Thu May 22 14:32:34 1997; MasPar time 5.02 Seconds

Tabular output not generated.

Title: >US-08-436-265-6
Description: (1-532) from US08436265.pep
Perfect Score: 3981

Sequence: 1 MTQLYIYIRLLGAYLFIISR.....TALRIKKTLLAKMVESQDVKI 532

Scoring table: PAM 150
Gap 11

Searched: 35845 seqs, 32290575 residues

Post-processing: Minimum Match 0%
Listing First 45 summaries

Database: a-issued
1:51 2:52 3:53 4:54 5:55 6:PCT90 7:PCT91 8:PCT92 9:PCT93
10:PCT94 11:PCT95 12:PCT96

Result	Query	Match	Length	DB	ID	Description	Pred. No.	
1	3981	100.0	532	11	PCT-US95-0	Sequence 6,	Applicatio	0.00e+00
2	3900	98.0	532	10	PCT-US94-1	Sequence 2,	Applicatio	0.00e+00
3	2757	69.3	502	10	PCT-US94-1	Sequence 4,	Applicatio	4.14e-231
4	2757	69.3	502	11	PCT-US95-0	Sequence 8,	Applicatio	4.14e-231
5	1754	44.1	503	10	PCT-US94-1	Sequence 10,	Applicati	8.61e-142
6	1737	43.6	501	5	US-08-149-	Sequence 17,	Applicati	2.78e-140
7	1737	43.6	501	5	US-08-317-	Sequence 6,	Applicati	1.67e-131
8	1638	41.1	509	10	PCT-US94-1	Sequence 4,	Applicatio	8.54e-131
9	1630	40.9	509	11	PCT-US95-0	Sequence 14,	Applicati	2.37e-130
10	1625	40.8	509	5	US-08-149-	ALIGNMENTS		

Result	Query	Match	Length	DB	ID	Description	Pred. No.
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98	PCT-US94-10080-2	1	STANDARD;	PRT;	532 AA.		
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101	PCT-US94-10080-2	1	STANDARD;	PRT;	532 AA.		
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127	PCT-US94-10080-2	1	STANDARD;	PRT;	532 AA.		

Searched: 333249 seqs, 555961234 bases x 2
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: emb1-new11
1:BCT 2:FUN 3:GEN 4:HUM1 5:HUM2 6:HUM3 7:INV1 8:INV2
9:INV3 10:INV4 11:INV5 12:INV6 13:INV7 14:ORG 15:MAM
16:VRT 17:PLN 18:PRO1 19:PRO2 20:ROD 21:SYN 22:UNC
23:VRT1 24:VRT2

Database: genbank97
25:BCT1 26:BCT2 27:BCT3 28:BCT4 29:BCT5 30:BCT6 31:BCT7
32:BCT8 33:BCT9 34:GEN1 35:GEN2 36:HTG 37:INV1 43:INV2
39:INV3 40:INV4 41:INV5 42:INV6 43:INV7 44:INV8 45:INV9
46:MAM1 47:MAM2 48:MAM3 49:VRT1 50:VRT2 51:VRT3 52:VRT1
53:VRT2 54:VRT3 55:VRT4 56:PHG 57:PLN1 58:PLN2 59:PLN3
60:PLN4 61:PLN5 62:PLN6 63:PLN7 64:PLN8 65:PLN9 66:PLN10
67:PR1 68:PR12 69:PR13 70:PR14 71:PR15 72:PR16 73:PR17
74:PR18 75:PR19 76:PR110 77:PR111 78:PR112 79:PR113
80:PR114 81:ROD1 82:ROD2 83:ROD3 84:ROD4 85:ROD5 86:ROD6
87:ROD7 88:ROD8 89:STR 90:SYN 91:UNA 92:VRL1 93:VRL2
94:VRL3 95:VRL4 96:VRL5 97:VRL6 98:VRL7 99:VRL8 100:VRL9

Database: genbank-new11
101:BCT 102:GEN 103:INV1 104:INV2 105:MAM 106:VRT
107:PHG 108:PLN 109:PR1 110:PR12 111:ROD 112:SYN
113:UNA 114:VRL
u-emb148_97
115:part1 116:part2

Database: Statistics: Mean 12.028; Variance 5.236; scale 2.297
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description	Pred. No.
1	1973	95.3	2292	84	MUSBMPRC		Mouse mRNA for BMP receptor Mus musculus type I	0.00e+00
2	1795	86.7	2402	82	MMU04672		Mouse mRNA for BMP receptor Mus musculus NIH3T3	0.00e+00
3	1665	80.4	2056	82	MMU04673		Mouse mRNA for BMP receptor Mus musculus NIH3T3	0.00e+00
4	1647	79.6	3167	88	S75359		Mouse mRNA for BMP receptor Mus musculus NIH3T3	0.00e+00
5	1539	77.2	1599	81	MMALK3A		Mouse mRNA for BMP receptor Mus musculus NIH3T3	0.00e+00
6	1564	75.6	2620	20	S74037		Mouse mRNA for BMP receptor Mus musculus NIH3T3	0.00e+00
7	1564	75.6	3003	87	RATRALK3		Rat mRNA for BMP receptor Mus musculus NIH3T3	0.00e+00
8	1564	75.6	3003	20	RNRAK3		Rat mRNA for BMP receptor Mus musculus NIH3T3	0.00e+00
9	1457	70.4	1599	87	RATRBR4R1		Rat mRNA for BMP receptor Mus musculus NIH3T3	0.00e+00
10	1417	68.5	2932	70	HSALK3A		Human mRNA for BMP receptor Mus musculus NIH3T3	0.00e+00

RESULT 1 MUSBMPRC 2292 bp mRNA ROD 25-NOV-1994
DEFINITION Mouse mRNA for BMP receptor, complete cds.
ACCESSION D16250
NID 9577633
KEYWORDS BMP receptor.
ORGANISM Mus musculus
SOURCE mRNA, clone mTR11-45.

RESULT 2 MUSBMPRC 2292 bp mRNA ROD 25-NOV-1994
DEFINITION Mouse mRNA for BMP receptor, complete cds.
ACCESSION D16250
NID 9577633
KEYWORDS BMP receptor.
ORGANISM Mus musculus
SOURCE mRNA, clone mTR11-45.

RESULT 3 MUSBMPRC 2292 bp mRNA ROD 25-NOV-1994
DEFINITION Mouse mRNA for BMP receptor, complete cds.
ACCESSION D16250
NID 9577633
KEYWORDS BMP receptor.
ORGANISM Mus musculus
SOURCE mRNA, clone mTR11-45.
TITLE A truncated bone morphogenetic protein receptor affects dorsal-ventral patterning in the early Xenopus embryo

Query Match 95.3%; Score 1973; DB 84; Length 2292;
Best Local Similarity 99.7%; Pred. No. 0.00e+00;
Matches 1993; Conservative 0; Mismatches 2; Indels 3; Gaps 3;

RESULT 2 MMU04672 2402 bp mRNA ROD 17-SEP-1994
LOCUS Mus musculus type I receptor BRK-1 mRNA, complete cds.
DEFINITION Mus musculus type I receptor BRK-1 mRNA, complete cds.
ACCESSION U04672
NID 9538362
KEYWORDS BRK-1; bone morphogenetic protein receptor kinase-1; full-length receptor protein kinase.
SOURCE house mouse.
ORGANISM Murinae; Mus.
Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata; Myomorpha; Muridae; Vertebrata; Eutheria; Rodentia; Sciurognath; Sciurognath; Muridae;
Murinae; Mur. 1 (bases 1 to 2402)
REFERENCE Koenig, B.B., Cook, J.S., Wolsing, D.H., Ting, J.J., Tiesman, J.P., Correa, P.E., Olson, C.A., Pequett, A.L., Ventura, F., Grant, R.A., Chen, G., Wrana, J.L., Massague, J., and Rosenbaum, J.S.
AUTHORS
TITLE Characterization and cloning of a putative receptor for BMP-2 and BMP-4 from NIH3T3 cells
JOURNAL Mol. Cell. Biol. 14, 5961-5974 (1994)
MEDLINE 9434106
REFERENCE 2 (bases 1 to 2402)
AUTHORS Rosenbaum, J.S.
TITLE Direct Submission
JOURNAL Submitted (22-DEC-1993) Jan S. Rosenbaum, The Procter & Gamble Company, Miami Valley Laboratories, P.O. Box 398707, Cincinnati, OH 45239-8707, USA
MEDLINE 9434106
REFERENCE 3 (bases 1 to 2402)
AUTHORS Rosenbaum, J.S.
TITLE Direct Submission
JOURNAL Submitted (22-DEC-1993) Jan S. Rosenbaum, The Procter & Gamble Company, Miami Valley Laboratories, P.O. Box 398707, Cincinnati, OH 45239-8707, USA
MEDLINE 9434106
REFERENCE 4 (bases 1 to 2402)
AUTHORS Rosenbaum, J.S.
TITLE Direct Submission
JOURNAL Submitted (22-DEC-1993) Jan S. Rosenbaum, The Procter & Gamble Company, Miami Valley Laboratories, P.O. Box 398707, Cincinnati, OH 45239-8707, USA
MEDLINE 9434106
REFERENCE 5 (bases 1 to 1599)
AUTHORS Miyazono, K.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-1993) Kohei Miyazono, Ludwig Institute for Cancer Research, Biomedical Center, Uppsala, S-751 24, Sweden
MEDLINE 95269711
REFERENCE 2 (bases 1 to 1599)
AUTHORS Dewulf, N., Verschueren, K., Lonnay, O., Moret, A., Grimsby, S., Vandie Spiegel, K., Miyazono, K., Huylebroeck, D., and Ten Dijke, P.
TITLE Distinct spatial and temporal expression patterns of two type I receptors for bone morphogenetic proteins during mouse embryogenesis
JOURNAL Endocrinology 136 (6), 2652-2663 (1995)
MEDLINE 95269711

Query Match 77.2%; Score 1599; DB 81; Length 1599;
Best Local Similarity 100.0%; Pred. No. 0.00e+00;
Matches 1599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
TITLE A truncated bone morphogenetic protein receptor affects dorsal-ventral patterning in the early Xenopus embryo

RESULT 6 ID S74037 backbone; RNA; ROD 2620 BP.

AC S74037; D38082;	NI 9765229	REFERENCE 2 (bases 1 to 2932)
DT 26-AUG-1996 (Rel. 49, Created)	DT 26-AUG-1996 (Rel. 49, Last updated, Version 1)	AUTHORS ten Dijke, P.P.
DT bone morphogenetic protein type IA receptor [rats, Wistar, dental pulp cell line RPC-C2A, mRNA, 2620 nt].	DT Submitted (06-APR-1993) Peter P ten Dijke, Ludwig Institute for Cancer Research, Uppsala, branch, Biomedical Center, Husargatan 3, Uppsala, S-751 24, Sweden	TITLE Activin receptor-like kinases: a novel subclass of cell-surface receptors with predicted serine/threonine kinase activity
KW Rattus sp. (rat)	REFERENCE 3 (bases 1 to 2932)	AUTHORS ten Dijke, P., Ichijo, H., Heldin, C.H. and Miyazono, K.
OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.	JOURNAL Toyoshima, H., Heldin, C.H. and Miyazono, K.	JOURNAL Cancer Research, Uppsala, branch, Biomedical Center, Husargatan 3, Uppsala, S-751 24, Sweden
[1]	TITLE Oncogene 8 (10), 2879-2887 (1993)	TITLE Activin receptor-like kinases: a novel subclass of cell-surface receptors with predicted serine/threonine kinase activity
RP 1-2620	JOURNAL Mpsrch_nn	JOURNAL Oncogene 8 (10), 2879-2887 (1993)
RX MEDLINE: 95032096.	MEMLINE: 95032096.	MEMLINE: 95032096.
RA Takeda K., Oida S., Ichijo H., Iimura T., Maruoka Y., Amagasa T., Sasaki S.;	RA n.a. - n.a. database search, using Smith-Waterman algorithm	RA n.a. - n.a. database search, using Smith-Waterman algorithm
RT "Molecular cloning of rat bone morphogenetic protein (BMP) type IA receptor and its expression during ectopic bone formation induced by BMP";	Run on: Thu Jun 26 01:22:24 1997;	Run on: Thu Jun 26 01:22:24 1997;
RL Biophys. Res. Commun. 204:203-209 (1994).	RESULTS 8	RESULTS 8
OS ID RNRALK3 standard; RNA; ROD; 3003 BP.	ID D38082;	ID D38082;
AC 91398909	AC 91398909	AC 91398909
DA 01-DEC-1994	DA 01-DEC-1994	DA 01-DEC-1994
DT 08-SEP-1996 (Rel. 42, Created)	DT 08-SEP-1996 (Rel. 49, Last updated, Version 3)	DT 08-SEP-1996 (Rel. 49, Last updated, Version 3)
DE Rat mRNA for bone morphogenetic protein type IA receptor, complete cds.	DE Rat mRNA for bone morphogenetic protein type IA receptor, complete cds.	DE Rat mRNA for bone morphogenetic protein type IA receptor, complete cds.
DE BMP receptor; bone morphogenetic protein type IA receptor; kinase; morphogenetic protein receptor; rALK-3; serine/threonine; transmembrane protein.	DE BMP receptor; bone morphogenetic protein type IA receptor; kinase; morphogenetic protein receptor; rALK-3; serine/threonine; transmembrane protein.	DE BMP receptor; bone morphogenetic protein type IA receptor; kinase; morphogenetic protein receptor; rALK-3; serine/threonine; transmembrane protein.
KW Rattus norvegicus (rat)	KW Rattus norvegicus (rat)	KW Rattus norvegicus (rat)
OS Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.	OS Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.	OS Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
[1]	RN 1-3003	RN 1-3003
RP Oida S.;	RP Oida S.;	RP Oida S.;
RT	RT	RT
RL Submitted (26-AUG-1994) to the EMBL/GenBank/DBJ databases.	RL Submitted (26-AUG-1994) to the EMBL/GenBank/DBJ databases.	RL Submitted (26-AUG-1994) to the EMBL/GenBank/DBJ databases.
RL Shinichiro Oida, Faculty of Dent., Tokyo Medical and Dental University, Department of Biochemistry; 1-5-45 Yushima, Bunkyo-ku, Tokyo 113, Japan (Tel:03-3813-6111(ex.5126), Fax:03-5684-8047)	RL Shinichiro Oida, Faculty of Dent., Tokyo Medical and Dental University, Department of Biochemistry; 1-5-45 Yushima, Bunkyo-ku, Tokyo 113, Japan (Tel:03-3813-6111(ex.5126), Fax:03-5684-8047)	RL Shinichiro Oida, Faculty of Dent., Tokyo Medical and Dental University, Department of Biochemistry; 1-5-45 Yushima, Bunkyo-ku, Tokyo 113, Japan (Tel:03-3813-6111(ex.5126), Fax:03-5684-8047)
[2]	[2]	[2]
RP 1-3003	RP 1-3003	RP 1-3003
RX MEDLINE: 95032096.	RX MEDLINE: 95032096.	RX MEDLINE: 95032096.
RA Takeda K., Oida S., Ichijo H., Iimura T., Maruoka Y., Amagasa T., Sasaki S.;	RA Takeda K., Oida S., Ichijo H., Iimura T., Maruoka Y., Amagasa T., Sasaki S.;	RA Takeda K., Oida S., Ichijo H., Iimura T., Maruoka Y., Amagasa T., Sasaki S.;
RT "Molecular cloning of rat bone morphogenetic protein (BMP) type IA receptor and its expression during ectopic bone formation induced by BMP";	RT "Molecular cloning of rat bone morphogenetic protein (BMP) type IA receptor and its expression during ectopic bone formation induced by BMP";	RT "Molecular cloning of rat bone morphogenetic protein (BMP) type IA receptor and its expression during ectopic bone formation induced by BMP";
RL Biophys. Res. Commun. 204:203-209 (1994).	RL Biophys. Res. Commun. 204:203-209 (1994).	RL Biophys. Res. Commun. 204:203-209 (1994).
RESULTS 8	RESULTS 8	RESULTS 8
Query Match 75 %; Score 1564; DB 20; Length 3003;	Query Match 75 %; Score 1564; DB 20; Length 3003;	Query Match 75 %; Score 1564; DB 20; Length 3003;
Best Local Similarity 93.9%; Pred. No. 0.00e+00;	Best Local Similarity 93.9%; Pred. No. 0.00e+00;	Best Local Similarity 93.9%; Pred. No. 0.00e+00;
Matches 1727; Conservative 0; Mismatches 103; Indels 10; Gaps 5;	Matches 1727; Conservative 0; Mismatches 103; Indels 10; Gaps 5;	Matches 1727; Conservative 0; Mismatches 103; Indels 10; Gaps 5;
RESULT 10	RESULT 10	RESULT 10
LOCUS HSALK3A 2932 bp	LOCUS HSALK3A 2932 bp	LOCUS HSALK3A 2932 bp
DEFINITION H. sapiens ALK-3 mRNA.	DEFINITION H. sapiens ALK-3 mRNA.	DEFINITION H. sapiens ALK-3 mRNA.
ACCESSION 222535	ACCESSION 222535	ACCESSION 222535
NID 9404186	NID 9404186	NID 9404186
KEYWORDS ALK-3 gene, cell surface receptor; serine threonine kinase.	KEYWORDS ALK-3 gene, cell surface receptor; serine threonine kinase.	KEYWORDS ALK-3 gene, cell surface receptor; serine threonine kinase.
SOURCE human.	SOURCE human.	SOURCE human.
ORGANISM Homo sapiens	ORGANISM Homo sapiens	ORGANISM Homo sapiens
Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2932)	REFERENCE 1 (bases 1 to 2932)	REFERENCE 1 (bases 1 to 2932)
AUTHORS ten Dijke, P.P., Ichijo, H.H., Franzen, P.P., Schulz, P.P., Saras, J.J., Toyoshima, H.H., Heldin, C.C. and Miyazono, K.K.	AUTHORS ten Dijke, P.P., Ichijo, H.H., Franzen, P.P., Schulz, P.P., Saras, J.J., Toyoshima, H.H., Heldin, C.C. and Miyazono, K.K.	AUTHORS ten Dijke, P.P., Ichijo, H.H., Franzen, P.P., Schulz, P.P., Saras, J.J., Toyoshima, H.H., Heldin, C.C. and Miyazono, K.K.
TITLE Activin receptor-like kinases: a novel subclass of cell surface receptors with predicted serine/threonine kinase activity	TITLE Activin receptor-like kinases: a novel subclass of cell surface receptors with predicted serine/threonine kinase activity	TITLE Activin receptor-like kinases: a novel subclass of cell surface receptors with predicted serine/threonine kinase activity
RESULT 1	RESULT 1	RESULT 1
ID Q66640 standard; CDNA: 2070 BP.	ID Q66640 standard; CDNA: 2070 BP.	ID Q66640 standard; CDNA: 2070 BP.
AC Q66640;	AC Q66640;	AC Q66640;
DT 20-JAN-1995 (first entry)	DT 20-JAN-1995 (first entry)	DT 20-JAN-1995 (first entry)
DE Mouse Activin receptor-like kinase 3 (mALK-3) CDNA.	DE Mouse Activin receptor-like kinase 3 (mALK-3) CDNA.	DE Mouse Activin receptor-like kinase 3 (mALK-3) CDNA.
KW serine threonine kinases; activin receptors; Act-R; superfamily;	KW serine threonine kinases; activin receptors; Act-R; superfamily;	KW serine threonine kinases; activin receptors; Act-R; superfamily;
ALIGNMENTS	ALIGNMENTS	ALIGNMENTS

proteins are soluble and will be excreted into supernatant by recombinant mammalian cells expressing them. Such cells can be delivered in a medium or matrix which partially impedes their mobility, thereby localising the cells to a site of bone or cartilage injury 1813 BP; 506 A; 397 C; 439 G; 471 T; SQ Sequence

Query Match 74.3%; Score 1538; DB 14; Length 1813; Best Local Similarity 94.4%; Pred. No. 0.00e+00; Matches 1882; Conservative 0; Mismatches 90; Indels 9; Gaps 4;

MPSrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Thu Jun 26 01:26:17 1997; MasPar time 1317.77 Seconds 1006.977 Million cell updates/sec

Tabular output not generated.

Title: >US-08-436-265-13
(1-2070) from US08436265.seq

Description: 2070 1 ATTCAAGATGGAAAGATA.....TTTGCCTTTTGTGTGT 2070
N.A. Sequence: Comp: TAAGTACTCTACCTCTGGTAT.....AAACGAAAAAAACAAACAA

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 887282 seqs, 320523884 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: EST-STS

Result No.	Query	Score	Match	Length	DB	ID	Description	Pred. No.
1	328	15.8	404	165	W39552	zc18g04_r1	Soares par	0.00e+00
2	237	11.4	285	93	MMTEST73.0	M.musculus	expressed	0.00e+00
3	231	11.2	259	38	H33315	EST109182	Rattus sp.	0.00e+00
4	208	10.0	263	116	N88732	K530b	Fetal heart,	0.00e+00
5	142	6.9	471	164	W34981	mc33h08_r1	Soares mou	5.03e+223
6	141.	6.8	739	10	AA053838	zf53c07_r1	Soares ret	5.78e-221
7	141	6.8	739	231	HSA53838	zf53c07_r1	Soares ret	5.78e-221
8	104	5.0	515	43	C17679	Human	placenta cDNA 5	8.01e-146
9	104	5.0	515	239	HSC6799	Human	placenta cDNA 5	8.01e-146
10C	100	4.8	357	65	HSC22ZA051	H. sapiens	partial cDNA 5	7.28e-138
11	96	4.6	211	61	HSC0HE101	H. sapiens	partial cDNA 5	6.02e-130

MPSrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Sat May 24 07:06:02 1997; MasPar time 70.46 Seconds 839.881 Million cell updates/sec

Tabular output not generated.

Title: >US-08-436-265-13
(1-2070) from US08436265.seq

Description: 2070 1 ATTATGAGATGGAAAGATA.....TTTGCCTTTTGTGTGT 2070
N.A. Sequence: Comp: TAAGTACTCTACCTCTGGTAT.....AAACGAAAAAAACAAACAA

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 53119 seqs, 14293498 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: n-issued 1:51 2:52 3:53 4:54 5:55 6:PCT90 7:PCT91 8:PCT92 9:PCT93 10:PCT94 11:PCT95 12:PCT96

Statistics: Mean 9.280; Variance 5.006; scale 1.854

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description	Pred. No.
1	1538	74.3	1813	10	PCT-US94-1	Sequence 1	Smith-Waterman algorithm	0.00e+00
2	1417	68.5	2932	11	PCT-US95-0	Sequence 5	Smith-Waterman algorithm	0.00e+00
3	520	25.1	1952	11	PCT-US95-1	Sequence 7	Smith-Waterman algorithm	0.00e+00
4	516	24.9	2076	10	PCT-US94-1	Sequence 3	Smith-Waterman algorithm	0.00e+00
5	259	12.5	1794	10	PCT-US94-1	Sequence 9	Smith-Waterman algorithm	2.46e-174
6	252	12.2	1506	5	US-08-317-	Sequence 4	Smith-Waterman algorithm	6.84e-69
7	253	12.2	1506	5	US-08-149-	Sequence 4	Smith-Waterman algorithm	6.84e-169
8	243	11.7	1647	10	PCT-US94-1	Sequence 7	Smith-Waterman algorithm	1.14e-69
9	243	11.7	1506	5	US-08-149-	Sequence 2	Smith-Waterman algorithm	6.70e-162
10	243	11.7	1506	5	US-08-317-	Sequence 2	Smith-Waterman algorithm	6.70e-162

ALIGNMENTS

RESULT 1

ID PCT-US94-10080-1 STANDARD; DNA; UNC; 1813 BP.

AC xxxxxxxx

DT 01-JAN-1900

DE Sequence 1, Application PC/TUS9410080.

CC Sequence 1, Application PC/TUS9410080.

CC GENERAL INFORMATION:

CC APPLICANT: GENETICS INSTITUTE, INC.

CC NUMBER OF SEQUENCES: 19

CC CORRESPONDENCE ADDRESS:

CC Query Match 74.3%; Score 1538; DB 10; Length 1813;

CC Best Local Similarity 94.4%; Pred. No. 0.00e+00;

CC Matches 1682; Conservative 0; Mismatches 90; Indels 9; Gaps 4;

CC APPLICANT:

CC TITLE OF INVENTION: RECEPTOR PROTEINS

CC NUMBER OF SEQUENCES: 19

CC CORRESPONDENCE ADDRESS:

CC Query Match 74.3%; Score 1538; DB 10; Length 1813;

CC Best Local Similarity 94.4%; Pred. No. 0.00e+00;

CC Matches 1682; Conservative 0; Mismatches 90; Indels 9; Gaps 4;

CC APPLICANT:

CC TITLE OF INVENTION: RECEPTOR PROTEINS

CC NUMBER OF SEQUENCES: 19

CC CORRESPONDENCE ADDRESS:

CC Query Match 74.3%; Score 1538; DB 10; Length 1813;

CC Best Local Similarity 94.4%; Pred. No. 0.00e+00;

CC Matches 1682; Conservative 0; Mismatches 90; Indels 9; Gaps 4;

CC APPLICANT:

CC TITLE OF INVENTION: MORPHOGENIC PROTEIN-SPECIFIC CELL

CC Sequence 5, Application PC/TUS9505467.

CC GENERAL INFORMATION:

CC APPLICANT:

CC TITLE OF INVENTION: SURFACE RECEPTORS AND USES THEREFOR

CC MPSrch_nn protein - protein database search, using Smith-Waterman algorithm

CC Run on:

CC Tabular output not generated.

CC Title:

CC Description: >US-08-436-265-14
(1-532) from US08436265.seq

CC Perfect Score: 3.986

CC Sequence:

CC MPSrch_nn protein - protein database search, using Smith-Waterman algorithm

CC Run on:

CC Tabular output not generated.

CC Title:

CC Description: >US-08-436-265-14
(1-532) from US08436265.seq

CC Perfect Score: 3.986

CC Sequence:

CC MPSrch_nn protein - protein database search, using Smith-Waterman algorithm

CC Run on:

CC Tabular output not generated.

CC Title:

CC Description: >US-08-436-265-14
(1-532) from US08436265.seq

CC Perfect Score: 3.986

CC Sequence:

CC MPSrch_nn protein - protein database search, using Smith-Waterman algorithm

CC Run on:

CC Tabular output not generated.

CC Title:

CC Description: >US-08-436-265-14
(1-532) from US08436265.seq

CC Perfect Score: 3.986

CC Sequence:

CC MPSrch_nn protein - protein database search, using Smith-Waterman algorithm

CC Run on:

CC Tabular output not generated.

CC Title:

CC Description: >US-08-436-265-14
(1-532) from US08436265.seq

CC Perfect Score: 3.986

CC Sequence:

CC MPSrch_nn protein - protein database search, using Smith-Waterman algorithm

CC Run on:

CC Tabular output not generated.

CC Title:

CC Description: >US-08-436-265-14
(1-532) from US08436265.seq

CC Perfect Score: 3.986

CC Sequence:

CC MPSrch_nn protein - protein database search, using Smith-Waterman algorithm

CC Run on:

CC Tabular output not generated.

CC Title:

CC Description: >US-08-436-265-14
(1-532) from US08436265.seq

CC Perfect Score: 3.986

CC Sequence:

CC MPSrch_nn protein - protein database search, using Smith-Waterman algorithm

CC Run on:

CC Tabular output not generated.

CC Title:

CC Description: >US-08-436-265-14
(1-532) from US08436265.seq

CC Perfect Score: 3.986

CC Sequence:

CC MPSrch_nn protein - protein database search, using Smith-Waterman algorithm

CC Run on:

CC Tabular output not generated.

CC Title:

CC Description: >US-08-436-265-14
(1-532) from US08436265.seq

CC Perfect Score: 3.986

CC Sequence:

CC MPSrch_nn protein - protein database search, using Smith-Waterman algorithm

CC Run on:

CC Tabular output not generated.

CC Title:

CC Description: >US-08-436-265-14
(1-532) from US08436265.seq

CC Perfect Score: 3.986

CC Sequence:

CC MPSrch_nn protein - protein database search, using Smith-Waterman algorithm

CC Run on:

CC Tabular output not generated.

CC Title:

CC Description: >US-08-436-265-14
(1-532) from US08436265.seq

CC Perfect Score: 3.986

CC Sequence:

CC MPSrch_nn protein - protein database search, using Smith-Waterman algorithm

CC Run on:

CC Tabular output not generated.

CC Title:

CC Description: >US-08-436-265-14
(1-532) from US08436265.seq

CC Perfect Score: 3.986

CC Sequence:

CC MPSrch_nn protein - protein database search, using Smith-Waterman algorithm

CC Run on:

CC Tabular output not generated.

CC Title:

CC Description: >US-08-436-265-14
(1-532) from US08436265.seq

CC Perfect Score: 3.986

CC Sequence:

CC MPSrch_nn protein - protein database search, using Smith-Waterman algorithm

CC Run on:

CC Tabular output not generated.

CC Title:

CC Description: >US-08-436-265-14
(1-532) from US08436265.seq

CC Perfect Score: 3.986

CC Sequence:

CC MPSrch_nn protein - protein database search, using Smith-Waterman algorithm

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CC Description: >US-08-436-265-14
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CC MPSrch_nn protein - protein database search, using Smith-Waterman algorithm

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CC Tabular output not generated.

CC Title:

CC Description: >US-08-436-265-14
(1-532) from US08436265.seq

CC Perfect Score: 3.986

CC Sequence:

CC MPSrch_nn protein - protein database search, using Smith-Waterman algorithm

• Searched: 92623 seqs, 10896596 residues
 Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database:	a-geneseq26 1:part1 2:part2 3:part3 4:part4 5:parts 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19
Statistics:	Mean 36.022; Variance 149.415; scale 0.241
Pred. No.	is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
SUMMARIES	
Result No.	Query Score Match Length DB ID Description Pred. No.
1	3986 100.0 532 19 R95225 Mouse BMP type I rece 0.00e+00
2	3986 100.0 532 17 R96201 Bone morphogenetic pr 0.00e+00
3	3986 100.0 532 13 R74343 BRK-1 protein. 0.00e+00
4	3961 99.4 532 13 R70237 Bone morphogenetic prot 0.00e+00
5	3915 98.2 532 14 R85207 Human ALK-3. 0.00e+00
6	3915 98.2 532 10 R55368 Human Activin recepto 0.00e+00
7	3686 92.5 500 13 R74342 Truncated BRK-1. 0.00e+00
8	2756 69.1 502 14 R85206 Mouse ALK-6. 6.0e-267
9	2756 63.1 502 13 R70238 Bone morphogenetic prot 6.0e-267
10	2746 68.9 502 19 R95226 Chick BMP type I rece 6.56e-266
ALIGNMENTS	
Result 1	Query R95225 standard; Protein: 532 AA.
ID R95225;	AC R95225;
DT 21-DEC-1996	(first entry)
DE Mouse BMP type I receptor kinase protein (BRK-1).	
KW BMP type II receptor kinase-3; BRK-3; bone morphogenetic protein;	
KW BMP type I receptor kinase; BRK-1; BMP receptor.	
OS Mus sp.	
PN W09614579-A1.	
PD 17-MAY-1996.	
PF 30-OCT-1995;	U14027.
PR 04-NOV-1994;	US-334178.
PR 05-JUN-1995;	US-462467.
PR (PROC) PROCTER & GAMBLE CO.	
PR Rosenbaum JS;	
DR WPI; 96-251687/25.	
DR T95225.	
PT Assays for bone morphogenetic protein activities - using complex of BMP type I receptor kinase protein and BMP receptor kinase protein BRK-3.	
PT Claim 2; Page 66-67; 101pp; English.	
PS Full-length mouse bone morphogenetic protein (BMP) type I receptor kinase protein-1 (BRK-1) (R95225) is a receptor capable of binding BMP and transducing a signal initiated by the binding. Its amino acid sequence was deduced from a cDNA clone (T28021). A BMP receptor kinase protein complex formed of full-length, incomplete or soluble BMP type I receptor kinase protein and full-length, incomplete or soluble BMP type II receptor kinase-3 (BRK-3) (see also R95222-24 and R9526-34) is useful for screening cDNA for BMP receptor affinity or for determining the concentration of a BMP receptor ligand in a clinical sample. The complex can be expressed by host cells co-transfected with vectors carrying the appropriate DNA sequences (see also T28018-30).	
SQ Sequence 532 AA;	

RESULT 2	ID R96201 standard; Protein; 532 AA.
AC R96201;	
DT 22-AUG-1996	(first entry)
DE Bone morphogenetic protein type-I receptor kinase-1.	
KW Mouse, bone morphogenetic protein receptor kinase-1; bone morphogenetic protein receptor kinase-3; antibody; diagnostic; bone disorder; osteogenic; bone morphogenetic protein-agonist; drug screening; reporter gene; bone morphogenetic protein-antagonist; hormone-responsive element.	
KW Mus musculus.	
OS Mus musculus.	
FH Key Location/Qualifiers	
FT Peptide 216..221	
FT /note= "Conserved BRK-1 motif"	
FT Peptide 398..421	
FT /note= "Peptide used to raise antibody"	
	PN W09614412-A2.
	PD 17-MAY-1996.
	PF 30-OCT-1995; U14085.
	PR 04-NOV-1994; US-334179.
	PA (PROC) PROCTER & GAMBLE CO.
	PI Nohno T, Rosenbaum JS;
RESULT 3	ID R74343 standard; Protein; 532 AA.
	AC R74343;
	FT 01-NOV-1995 (first entry)
	FT BRK-1 protein.
	FT DE BRK-1 protein.
	KW BMP receptor kinase protein-1; bone morphogenetic protein.
	OS Mus sp.
	FH Key Location/Qualifiers
	FT Peptide 1..23
	FT /label= Sig_peptide
	FT Domain 24..152
	FT /label= Extracellular_ligand_binding_domain
	FT Domain 153..176
	FT /label= Transmembrane_domain
	FT Domain 177..532
	FT /label= Intracellular_kinase_domain
	PN W09514778-A.
	PD 01-JUN-1995.
	PF 23-NOV-1994; U13534.
	PR 24-NOV-1993; US-158735.
	PA (PROC) PROCTER & GAMBLE CO.
	PI Cook JS, Correa PE, Koenig BB, Rosenbaum JS, Ting J;
	DR WPI; 95-206235/27.
	DR N-PSDB; Q90184.
	PT New bone morphogenetic protein receptor kinase protein - used for identifying cDNA capable of binding it and for developing therapeutic
	PT cDNA and detection system(s)
	PT Claim 1; Page 29-32; 49pp; English.
	CC A cDNA library prepared from NIH3T3 poly-A RNA was screened with PCR fragment to isolate clone BRK-1 (sequence given in Q90184) encoding full-length BMP receptor kinase protein (R74343).
	CC Vectors including the DNA were used to express recombinant BRK-1 in CHO and COS-7 hosts.
	SQ Sequence 532 AA;
RESULT 4	ID R70237 standard; Protein; 532 AA.
AC R70237;	
DT 28-SEP-1995	(first entry)
DE Bone morphogenetic protein receptor CFK1-23a.	
KW Bone morphogenetic protein; receptor; serine/threonine kinase; BMP;	
Query Match 100.0%; Score 3986; DB 13; Length 532;	
Best Local Similarity 100.0%; Pred. No. 0.00e+00;	
Matches 532; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	

QY 481 PIVSNRWNNSDECRLAVLKLIMSECWAHNPASRLTALRIKKTIAKMVESQDVKI 532

MPSrch_PP Protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Jun 24 17:52:10 1997; MasPar time 19.41 Seconds

Perfect Score: 3986

Sequence: 1 MTQLYTYIRLIGACLFISH. TALRIKKTIAKMVESQDVKI 532

Scoring table: PAM 150

Gap 11

Searched: 89912 seqs, 28507787 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

pir50

1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
13:unann9 14:unann10 15:unenc 16:unrev

Database: [REDACTED]

Statistics: Mean 48.972; Variance 115.254; scale 0.4225

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.	
1	3986	100.0	532	14	A56238	bone morphogenetic P	0.00e+00
2	3962	99.4	532	14	JC2387	bone morphogenetic P	0.00e+00
3	3915	98.2	532	13	S37183	ALK-3 protein - huma	0.00e+00
4	3915	98.2	532	13	I37163	ALK-3 - human	0.00e+00
5	3686	92.5	500	14	B56238	bone morphogenetic P	0.00e+00
6	3124	78.4	527	12	A54985	BMP receptor precurs	0.00e+00
7	2756	69.1	502	14	A53444	activin receptor-lik	0.00e+00
8	2756	69.1	502	14	JC2491	serine/threonine kin	0.00e+00
9	2746	68.9	502	13	A56683	receptor protein kin	0.00e+00
10	1770	44.4	503	13	A49432	activin receptor-lik	1.52e-283
11	1763	44.2	503	14	JC2061	transforming growth	2.75e-282

ALIGNMENTS

RESULT 1 ENTRY A56238 #type complete

TITLE bone morphogenetic protein receptor BRK-1 - mouse

ALTERNATE_NAMES ALK-3 protein; BMP receptor

ORGANISM #formal name *Mus musculus* #common name house mouse

DATE 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 06-Sep-1996

ACCESSIONS A56238; S40158; I48242; I49543

REFERENCE A56238

#authors Koenig, B.B.; Cook, J.S.; Wolsing, D.H.; Ting, J.; Tiesman, F.; Grant, R.A.; Olson, C.A.; Pecquet, A.L.; Ventura, J.P.; Rosenbaum, J.S.

Mol. Cell. Biol. (1994) 14:5961-5974

Characterization and cloning of a receptor for BMP-2 and BMP-4 from NIH 3T3 cells.

#journal A56238

#status preliminary

#molecule_type mRNA

#residues 1-532 #label KOE

#cross-references GB:U04672

RESULT 1 ENTRY A56238 #type complete

TITLE bone morphogenetic protein receptor TAK

ALTERNATE_NAMES 1-532 #label TAK

ORGANISM #formal name *Rattus norvegicus* #common name Norway rat

DATE 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Jan-1996

ACCESSIONS JC2387

REFERENCE JC2387

#authors Takeda, K.; Oida, S.; Ichijo, H.; Iimura, T.; Maruoka, Y.;

Amagasa, T.; Sasaki, S.

#journal Biochem. Biophys. Res. Commun. (1994) 204:203-209

Molecular cloning of rat bone morphogenetic protein (BMP) type IA receptor and its expression during ectopic bone formation induced by BMP.

#accession JC2387

#molecule_type mRNA

#residues 1-532 #label TAK

#cross-references DBJ:D38082

CLASSIFICATION #superfamily protein kinase homology glycoprotein; receptor; transmembrane protein

KEYWORDS 1-23 #product bone morphogenetic protein type IA receptor

#cross-references GB:U04672

#domain signal sequence #status predicted #label SIG\

#status predicted #label BMP\\
 #domain transmembrane #status predicted #label KIN\\
 #domain protein kinase homology #label KIN\\
 #region kinase domain\\
 #binding_site carbohydrate (Asn) (covalent) #status

SUMMARY #length 532 #molecular_weight 59994 #checksum 7758

RESULT 6 A54985 #type complete

ENTRY #BMP receptor precursor - African clawed frog

TITLE #informal name Xenopus laevis #common_name African clawed frog

ORGANISM 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change

DATE 08-Dec-1995

ACCESSIONS A54985

REFERENCE #authors Graft, J.M.; Thies, R.S.; Song, J.J.; Celeste, A.J.; Melton, D.A.

#journal Cell (1994) 79:169-179

#title Studies with a Xenopus BMP receptor suggest that ventral mesoderm-inducing signals override dorsal signals in vivo.

#accession A54985

#status preliminary; not compared with conceptual translation

#molecule_type mRNA

#residues 1-527 #label GRA

#note nucleotide sequence is not given

#superfamily protein kinase homology

#classification #superfamily protein kinase homology

FEATURE #domain protein kinase homology #label KIN

#length 527 #molecular_weight 59800 #checksum 7791

SUMMARY #length 523 #domain kinase homology #label KIN

Query Match 78.4%; Score 3124; DB 12; Length 527;

Best Local Similarity 79.9%; Pred. No. 0.00e+00;

Matches 421; Conservative 55; Mismatches 45; Indels 6; Gaps 4;

Db 6 fiacfga-lllvihtggdnfilphrgmksndpkqgengvtlapeditlpflncysgy 64

Qy 7 YIRLIGACLFIIISHVQGNLDSMLHGGMKSDLDQKPKENGVTLAPEDTLPLKCYCSGH 66

Db 65 cpqnavntcinqqcfaamieejngqiiitsgqmkmegsdfqgctsdspkalsrrteccr 124

Qy 67 CPDDAINTNTCITNGHCFAITEEDDQGETTLTSGCMKYEESDFOQKSPKAQHLRTTECCR 126

Db 125 tdfcnrdleptlspkisdegy--alrtfiaiislvvcilivgfiliiwiyh-khhsq 180

Qy 127 TNLCNQYLOPQTPPVIGPFDGSIWLVVLSMACIVAMIIFS SCFCYKHYCKSTSS 185

Db 181 rmlynrnldpddafipageslkalidisqssqsgsllvgrtiakqimvraqgkgy 240

Qy 186 RGGRYNRDLQEDEAFIPVGESKLDTDSQSSGSGSPGLIVQRTAKQIQMVRQVGGRY 245

Db 241 gevngqkwrgekvavkvvftaaeaswfrteiyqtvylmrhenilgqiaadikgtgswtqm 300

Qy 246 GEVNMGKWRGEKVAVKVFVFTTEASWFRTEIYQTVLMRHENILGFIADIKGTGSMTQL 305

Db 301 ylityehngslydflikctldtrslklaysaaaglchlteiygtqgkpaiahrlks 360

Qy 306 YLITDXHENGSLYDFLIKCATLDTRALKLAYSAAAGLCHLHTEYGTQGKPAIAHRLKS 365

Db 361 knlikewntcciadlglavkfnstdhevdplntrvgtkrymapvevdelslnkhfqay 420

Qy 366 KNLIKNGSCCIADLGAVKFNSDTNEVDIPLNTRVGTKRYMAPVEVDLSLANKNHFQPY 425

Db 421 imadysfsliiwmtrctitggiveeyqplyydmphpsfedrevenmkclp:ivsn 480

Qy 426 IMADYSFGLIWIWEMARCTIGGIVEYQPLYYNMVPSPSYEDNREVVWCVKRLRPIVSN 485

Db 481 rwnsdeclarvlklmaecwaqnpassltalrikktlakmvsesqavki 527

Qy 486 RWNSDDECLRAVILKLMSEWAHNPASRITALRIKKTLMVSEWVQVYKI 532

RESULT 7 A53444 #type complete

ENTRY #activin receptor-like kinase 6 precursor - mouse

TITLE #informal name Mus musculus #common_name house mouse

ORGANISM 19-May-1994 #sequence_revision 19-May-1994 #text_change

DATE 08-Dec-1995

ACCESSIONS A53444; S40159

REFERENCE #authors Graft, J.M.; Thies, R.S.; Song, J.J.; Celeste, A.J.; Melton, D.A.

#journal Cell (1994) 79:169-179

#title Studies with a Xenopus BMP receptor suggest that ventral mesoderm-inducing signals override dorsal signals in vivo.

#accession A53444

#status preliminary; not compared with conceptual translation

#molecule_type mRNA

#residues 1-500 #label KOE

#crosses-references GB-U04673

#note neither protein nor nucleotide sequence is given; it is unclear whether this clone represents a naturally occurring variant or an incompletely processed mRNA transcript

SUMMARY #length 500 #molecular_weight 56438 #checksum 4304

Query Match 92.5%; Score 3686; DB 14; Length 500;

Best Local Similarity 100.0%; Pred. No. 0.00e+00;

Matches 491; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ACCESSIONS

REFERENCE	A53444	ten Dijke, P.; Yamashita, H.; Ichijo, H.; Franzen, P.; Iaiho, M.; Miyazono, K.; Heldin, C.H.	Sequence 17, Application 1.03e-141
#authors		Science (1994) 264:101-104	Sequence 6, Application 1.79e-131
#journal		Characterization of type I receptors for transforming growth factor-beta and activin.	Sequence 4, Application 4.07e-131
#title	A53444		Sequence 14, Application 2.57e-130
#accession			
##status	preliminary		
##molecule_type	mRNA		
##residues	1-502	##label1 TEN	
##cross-references	GB:Z23143		
REFERENCE	S40158	Miyazono, K.; Moren, A.; Grimsby, S.; Ichijo, H.; Heldin, C. ten Dijke, P.	Sequence 2, Application PC/TUS9410080.
#authors		submitted to the EMBL Database Library, June 1993	XX
#description	ALK-3 and ALK-6: the closely related members in the serine/threonine kinase receptor family.	CC	GENERAL INFORMATION:
#accession	S40159		CC
##status	preliminary		CC
##molecule_type	mRNA		CC
##residues	1-502	##label1 MIY	CC
##cross-references	EMBL:Z23143		CC
CLASSIFICATION	#superfamily	protein kinase homology	CC
RE	24.98	#domain protein kinase homology #label KIN	CC
Query Match	#length 502	#molecular_weight 56944 #checksum 5099	CC
Best Local Similarity	69.1%	Score 2756; DB 14; Length 502;	Query Match: 99.4%;
Matches	364;	Pred. No. 0.00e+00; Conservative 76; Mismatches 60; Indels 5; Gaps 5;	Best Local Similarity: 98.9%;
Run on:	Thu May 22 14:34:01 1997;	MasPar time 4.89 Seconds	Matches: 526; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
SEARCH_PP	protein	- protein database search, using Smith-Waterman algorithm	RESULT 1
Query			ID PCT-US94-10080-2 STANDARD;
Run on:			XX
Tabular output not generated.			AC xxxxxxxx
Title:	>US-08-436-265-14		DE 01-JAN-1900
Description:	(1-532) from US08436265.pop		XX
Perfect Score:	3986		Sequence 6, Application PC/TUS9505467.
Sequence:	1 NTQLYTYIRLLGACLFIISH.....TALRIKKTLAKMVEQDVK1	532	CC
Scoring table:	PAM 150		GENERAL INFORMATION:
	Gap 11		CC
Searched:	35845 seqs,	3290575 residues	APPLICANT:
Processing:	Minimum Match 0%	LISTING FIRST 45 SUMMARIES	TITLE OF INVENTION: MORPHOGENIC PROTEIN-SPECIFIC CELL, SURFACE RECEPTORS AND USES THEREFOR
Database:	a-issued		NUMBER OF SEQUENCES: 15
	1:51 2:52 3:53 4:54 5:55 6:PCT90 7:PCT91 8:PCT92 9:PCT93		CC
	10:PCT94 11:PCT95 12:PCT96		Query Match 69.1%;
Statistics:	Mean 33.987; Variance 162.888; scale 0.209		Best Local Similarity 72.1%;
			Pred. No. 4.94e-232;
			CC
			Sequence 4, Application PC/TUS9410080.
			CC
			GENERAL INFORMATION:
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			NUMBER OF SEQUENCES: 19
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			Best Local Similarity 72.1%;
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			Sequence 4, Application PC/TUS9410080.
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			GENERAL INFORMATION:
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			TITLE OF INVENTION: RECEPTOR PROTEINS
			NUMBER OF SEQUENCES: 19
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			Query Match 69.1%;
			Best Local Similarity 72.1%;
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			Sequence 4, Application PC/TUS9410080.
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			APPLICANT: GENETICS INSTITUTE, INC.
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			TITLE OF INVENTION: RECEPTOR PROTEINS
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			Query Match 69.1%;
			Best Local Similarity 72.1%;
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			Sequence 4, Application PC/TUS9410080.
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			TITLE OF INVENTION: RECEPTOR PROTEINS
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			Sequence 4, Application PC/TUS9410080.
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			Best Local Similarity 72.1%;
			Pred. No. 4.94e-232;
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			Sequence 4, Application PC/TUS9410080.
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			Sequence 4, Application PC/TUS9410080.
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			NUMBER OF SEQUENCES: 19
			CC
			Query Match 69.1%;
			Best Local Similarity 72.1%;
			Pred. No. 4.94e-232;
			CC
			Sequence 4, Application PC/TUS9410080.
			CC
			GENERAL INFORMATION:
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			APPLICANT: GENETICS INSTITUTE, INC.
			CC
			TITLE OF INVENTION: RECEPTOR PROTEINS
			NUMBER OF SEQUENCES: 19
			CC
			Query Match 69.1%;
			Best Local Similarity 72.1%;
			Pred. No. 4.94e-232;
			CC
			Sequence 4, Application PC/TUS9410080.
			CC
			GENERAL INFORMATION:
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			APPLICANT: GENETICS INSTITUTE, INC.
			CC
			TITLE OF INVENTION: RECEPTOR PROTEINS
			NUMBER OF SEQUENCES: 19
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			Query Match 69.1%;
			Best Local Similarity 72.1%;
			Pred. No. 4.94e-232;
			CC
			Sequence 4, Application PC/TUS9410080.
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			GENERAL INFORMATION:
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			Sequence 4, Application PC/TUS9410080.
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			TITLE OF INVENTION: RECEPTOR PROTEINS
			NUMBER OF SEQUENCES: 19
			CC
			Query Match 69.1%;
			Best Local Similarity 72.1%;
			Pred. No. 4.94e-232;
			CC
			Sequence 4, Application PC/TUS9410080.
			CC
			GENERAL INFORMATION:
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			APPLICANT: GENETICS INSTITUTE, INC.
			CC
			TITLE OF INVENTION: RECEPTOR PROTEINS
			NUMBER OF SEQUENCES: 19
			CC
			Query Match 69.1%;
			Best Local Similarity 72.1%;
			Pred. No. 4.94e-232;
			CC
			Sequence 4, Application PC/TUS9410080.
			CC
			GENERAL INFORMATION:
			CC
			APPLICANT: GENETICS INSTITUTE, INC.
			CC
			TITLE OF INVENTION: RECEPTOR PROTEINS
			NUMBER OF SEQUENCES: 19
			CC
			Query Match 69.1%;
			Best Local Similarity 72.1%;
			Pred. No. 4.94e-232;
			CC
			Sequence 4, Application PC/TUS9410080.
			CC
			GENERAL INFORMATION:
			CC
			APPLICANT: GENETICS INSTITUTE, INC.
			CC
			TITLE OF INVENTION: RECEPTOR PROTEINS
			NUMBER OF SEQUENCES: 19
			CC
			Query Match 69.1%;
			Best Local Similarity 72.1%;
			Pred. No. 4.94e-232;
			CC
			Sequence 4, Application PC/TUS9410080.
			CC
			GENERAL INFORMATION:
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			Query Match 69.1%;
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Qy 89 DDDGETTLTSGCMKYEGLSDFQCKDPSKAQLRTIECCRT-NLCNQYLQPTLPPVIGPFF 147
Db 120 DGETHHKALLISTVTVSLLVLL-FCYFRY-KRQDARPRYSTGLEQDETYIPPGESLR 177
Qy 148 DGETRWLVYLLISMAVIVAMIFSSCFCYKHYCKSISRRGTYNRDLEQDAAFIYPGESLK 207
Db 178 DLIEQSOSSGSGSGLPLVORTIAKQIOMYKQIGKGRYGEVWNGKWRGEVAKVQFETTE 237
Qy 208 DLIDQSOSSGSGSGLPLVORTIAKQIOMYRQVKGGRYGEVWNGKWRGEVAKVQFETTE 267
Db 238 EASWFRETEIYQTVILMRHENILIGFTIAADIKGTGSWTOLYLTDYHENGSLYDYLKSTTLID 297
Qy 268 EASWFRETEIYQTVILMRHENILIGFTIAADIKGTGSWTOLYLTDYHENGSLYDYLKCATLID 327
Db 298 AKSMLKLAYSSVSGLCHLHTEIFSTQGKPAIAHRLDKSKNLLVKKNGTCCTADLGLAVKF 357
Qy 328 TRAILKLAYSAACGLCHLHTEIYGTQGKPAIAHDLKSKNLLIKKNGSCCTADLGLAVKF 387
Dr 358 ISDTNEVDIPLNTRVGTKRYMPEVILDESLNRTTHI2SYIMADMSFGLIWEIARCVSG 417
Qy 388 NSDTNEVDIPLNTRVGTKRYMPEVILDESLNKNHFQPYIMADISFGLIWEIARRCITG 447
Qy 418 GIVEEYQLPYHDLVPSDPSYEDMREIVCMKKLRLPSFPNRWSSEDECLRQMGKLMTECWAHN 477
Qy 448 GIVEEYQLPYNNMVPSPDPSYEDMREIVCMKKLRLPSFPNRWSSEDECLRQMGKLMTECWAHN 507
Db 478 PASRLTALRKYKTLAKNSSESDIKL 502
Qy 506 PASRLTALRKYKTLAKMVESQDVKI 532